

§Appl. No. 09/856,044  
Amdt. dated August 9, 2005  
Reply to Office Action of, May 10, 2005

### **REMARKS**

#### **Rejections under §112, second paragraph**

The claims have been amended to correct the inadvertent lapses in antecedent basis. These amendments do not change the scope of the claims.

#### **Rejections under §102 and §103**

Applicant respectfully traverses the rejection. Yates, *J. Mass Spec.*, 33:1-19 (1998) does not anticipate or render obvious the claims, either alone or in combination with additional references.

It is stated in the Office action that: "Yates III teaches a method for using sequence databases to identify amino acid sequence obtained by mass spectrometry wherein the database is searched for intact, undigested proteins (page 7, column 1, first full paragraph; page 7, column 2, last paragraph)."

This rejection does not appear to be proper. For example, the examiner pointed to Page 7, column 1, first full paragraph, and column 2, last paragraph, for disclosure of searching a database for intact, undigested proteins. However, the disclosure on Page 7, column 1, describes confirming the sequence of a known protein by comparing its predicted mass to its mass as determined by mass spectrometry. The pending claims distinguish over the disclosure on Page 7, column 1, at least because the claimed method is performed on a sample comprising "a plurality of proteins from one or more unknown microorganism" and the searching is used to identify one or more unknown organisms, not to confirm its sequence.

It is also alleged that Yates disclose "a sample that comprises a plurality of proteins from one or more unknown organisms (page 13, column 2-page 14, column 2)." However, Yates clearly states that a step of proteolysis is required in his method. The title of the section relied upon in the Office action is "'Shotgun' Identification of Proteins in Mixtures" which is described

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“as akin to a shotgun blast, creating many smaller fragments from a larger shell. The smaller fragments are analyzed and computer algorithms are then used to reconstruct the identities of the proteins...” Yates, 1998, Page 14, Column 1. Thus, the sample is comprised of fragments, not of intact, undigested proteins, and the fragments are analyzed, not intact undigested proteins.

Yates is also alleged to disclose “a database where molecular weight is deduced from nucleotide or protein sequence information (page 7, column 2, last paragraph – page 8, column 1 and Figure 3). However, in Figure 3, it is stated: “Peptide mass mapping. A protein sequence can be verified by site-specific digestion and measurement of the peptide ion ... Conversely, if the identify of the protein is not known the peptide map can be used to search the protein database ...” Moreover, the disclose expressly states “In 1993 five laboratories independently developed computer algorithms to use peptide mass maps to search protein databases and so identify proteins.” Thus, the examiner is correct that molecular weight is utilized by Yates and others, but it is the molecular weight of peptides obtained from proteolytic digestion of larger proteins.

Wang et al. and U.S. Pat. No. 5,538,897 (Yates) do not correct these deficiencies, and therefore they do not in combination with Yates render the claimed invention obvious. Neither of these references disclose or suggest searching a database for the molecular weights of a plurality of intact, undigested proteins.

In view of the above remarks, favorable reconsideration is courteously requested. If there are any remaining issues which could be expedited by a telephone conference, the Examiner is courteously invited to telephone counsel at the number indicated below.

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The Commissioner is hereby authorized to charge any fees associated with this response or credit any overpayment to Deposit Account No. 13-3402.

Respectfully submitted,



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